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OM nucleic - nucleic search, using sw model

Run on: February 16, 2003, 17:00:49 ; Search time 194.042 Seconds
(without alignments)
10829.323 Million cell updates/sec

Title: US-09-497-967-44
Perfect score: 1410

Sequence: 1 atgaaaaataatttttagt.....cttattattattatgatga 1410

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2773584 seqs, 745158349 residues

Total number of hits satisfying chosen parameters: 5547168

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database :
- 1: Pending Patents_NA_New.*
 - 2: /cgn2.6/ptodata/1/pna/PCT_NEW_COMB.seq.*
 - 3: /cgn2.6/ptodata/1/pna/US06_NEW_COMB.seq.*
 - 4: /cgn2.6/ptodata/1/pna/US07_NEW_COMB.seq.*
 - 5: /cgn2.6/ptodata/1/pna/US08_NEW_COMB.seq.*
 - 6: /cgn2.6/ptodata/1/pna/US09_NEW_COMB.seq.*
 - 7: /cgn2.6/ptodata/1/pna/US10_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	77.4	5.5	897	6	US-10-144-771-39592	Sequence 39592, A
2	65.4	4.6	961	6	US-10-144-771-31796	Sequence 31796, A
3	60	4.3	1635	6	US-10-203-138A-8641	Sequence 8641, Ap
4	60	4.3	1973	6	US-10-203-138A-3500	Sequence 3500, Ap
5	53.4	3.8	1188	6	US-10-144-771-4034	Sequence 4034, Ap
6	52.2	3.7	510	6	US-10-203-138A-7146	Sequence 7146, Ap
7	50	3.5	1248	6	US-10-092-411A-1120	Sequence 1120, Ap
8	49	3.5	1141	5	US-09-806-708B-22	Sequence 22, Appl
9	48	3.4	3532	6	US-10-017-161-1913	Sequence 1913, Ap
10	47.4	3.4	1954	6	US-10-144-771-4707	Sequence 4707, Ap
11	45.8	3.2	1075	6	US-10-203-138A-7632	Sequence 7632, Ap
12	45.8	3.2	1403	6	US-10-203-138A-2529	Sequence 2529, Ap
13	45.8	3.2	3489	6	US-10-194-046-1	Sequence 1, Appl
14	45.8	3.2	11091	6	US-10-092-411A-2243	Sequence 2243, Ap
15	45	3.2	21423	5	US-09-949-004-601	Sequence 601, Appl
16	44.4	3.1	583	6	US-10-144-771-29725	Sequence 29725, A
17	44.4	3.1	7040	6	US-10-311-506-48	Sequence 48, Appl
18	44.4	3.1	7040	6	US-10-311-506-48	Sequence 48, Appl
19	43.4	3.1	1231	6	US-10-017-161-2047	Sequence 2047, Ap
20	43.2	3.1	38918	6	US-10-017-161-2049	Sequence 2049, Ap
21	43.2	3.1	428573	5	US-09-948-124-119	Sequence 119, Appl
22	43	3.0	263	5	US-09-531-113-48328	Sequence 48328, A
23	42.8	3.0	439	6	US-10-203-138A-8573	Sequence 8573, Ap
24	42.8	3.0	1664976	5	US-09-692-570-1	Sequence 1, Appl
25	42.2	3.0	1805	6	US-10-144-771-22890	Sequence 22890, A
26	42.2	3.0	2323866	5	US-09-948-124-64	Sequence 64, Appl

RESULT 1
US-10-144-771-39592
; Sequence 39592, Application US/10144771
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
; FILE REFERENCE: CL001321
; CURRENT APPLICATION NUMBER: US/10/144,771
; CURRENT FILING DATE: 2002-05-15
; NUMBER OF SEQ ID NOS: 47235
; SEQ ID NO 39592
; LENGTH: 897
; TYPE: DNA
; ORGANISM: HUMAN
; US-10-144-771-39592

Query Match 5.5%; Score 77.4; DB 6; Length 897;
Best Local Similarity 43.9%; Pred. No. 4.3e+08;
Matches 330; Conservative 0; Mismatches 421; Indels 0; Gaps 0;

ALIGNMENTS

c	27	42	3.0	574	6	US-10-203-138A-227	Sequence 227, App
	28	42	3.0	3673778	6	US-10-312-841-1	Sequence 1, Appl
	29	41.8	3.0	756	7	US-60-434-832-6082	Sequence 6082, Ap
	30	41.8	3.0	9180	6	US-10-311-455-1937	Sequence 1937, Ap
c	31	41.8	3.0	17594	6	US-10-311-455-2000	Sequence 2000, Ap
	32	41.8	3.0	729	6	US-10-144-771-31479	Sequence 31479, A
	33	41.6	3.0	1118	6	US-10-144-771-33054	Sequence 33054, A
c	34	41.6	3.0	1141	5	US-09-531-113-35330	Sequence 22, Appl
c	35	41.2	2.9	203	5	US-09-806-708B-22	Sequence 35330, A
	36	41.2	2.9	1083	5	US-09-950-084-2103	Sequence 2103, Ap
c	37	41.2	2.9	1372	6	US-10-017-161-2245	Sequence 2245, Ap
c	38	41.2	2.9	3275	6	US-10-144-771-21113	Sequence 21113, A
	39	41.2	2.9	5912	6	US-10-311-455-575	Sequence 575, App
	40	41.2	2.9	6092	6	US-10-311-455-994	Sequence 994, App
c	41	41.2	2.9	74105	5	US-09-950-084-7446	Sequence 7446, Ap
c	42	41.2	2.9	580073	4	US-08-545-528D-1	Sequence 1, Appl
c	43	41	2.9	489	6	US-10-203-138A-5026	Sequence 5026, Ap
	44	41	2.9	1278	6	US-10-092-411A-58	Sequence 58, Appl
	45	41	2.9	2297	5	US-09-724-676-30403	Sequence 30403, A

Db 139 HHVYVAMNNAWTTTMCMDKDDKTRWWWKKNNAATGWDDDTKYHHWNNNGCBFTVVMVRY 198
QY 303 TGCAGGTGAGCAACAGATTGTCAGCAATAATACACAGAAATGTGTAATTTGAGAAATTA 362
Db 199 KTDSDSBRNNYMGWBWKNWSDVYIYVWDDCKRKVRWVRTGRMRNMYAWBTA 258
QY 363 TTTTATAATGAAATGCTCCAAATTTTAAATGAGGTGCTAGTACATGACAGACCTTGCC 422
Db 259 HRRRYNGWTBAMAYRRWTTNNNNNAKAMCKRAKYWGWNRAVNST-CTTWKSKTKVR 317
QY 423 GGTAAACAGAGTTGGTGGTGCATTGACTGCTGTAATGCCGTACCATAGTCGCATAATG 482
Db 318 TSWANNCRAGDANKHKKWWSAAGVYVNNNNNNNNWYKKARHBRWDVWHSNKKW 377
QY 483 TAACGTCGCTACTGCTACTGGTACTGCACCTTGATGATGAGTAACACTACTGATTATGTTAG 542
Db 378 HANAAYSRKKWTBYRKRTVMVNNNGTMMKRWAWYWKMDWBGTYNNNNGGRTYVG 437
QY 543 ATCAATTCACAGAATGTTAAATGCTAGACTTAACCTTTACTATAATGGAATAATGTA 602
Db 438 WTKNKKMTYTYWKANNCKRAWDHKTCTHNNTTWMMKTYMNNCYKWSKNTNGKSHRBA 497
QY 603 TACTCCTTTCAATCCAGGTAAAGTTAAATGCACACACTTGTCCGGCAATTAACCTGCTAA 662
Db 498 AVYTWYWWRRYAHANNWYVWRACITWYKYBVCWKNNVYAAWYTKSSWNTSKRYR 557
QY 663 TGTGCTTAAGCTACTTTAGTAATGCTACAATAACCGCATATGTAACCTTGCATG 722
Db 558 WKTNSNRWRSDDRSMGRANNYARAHYGYKWT RWBWSHTWBHBRAGAHHYMBWMBYB 617
QY 723 CCCTGATGTTACTAATGCTGCTGCTGAGTAATAATTTGGGTAGCACAAACACTGAATG 782
Db 618 AKCHMKAWTKAKYAGAGSNNNNNNNNNNNNNNNNATCARDYYAASRWYAMAKWY 677
QY 783 TACTAATTTGCTCCTCACTTTTACAATAATAATGCTCCTCAATTTCAATCCAGGTAAATG 842
Db 678 YKBAANNAYYTHANNWGCWNNATDRTRTWKNNNNNNAGTWKNNNNNNNAKNA 737
QY 843 TACATGCTACTTGGCCAGCAATAAGATTATGGTGGCTGAAGCCACTGCAGTGTGTC 902
Db 738 AAAAVKAAKHWANKWAMRGWADAAABTTDRKNGAYTKYTTNNNTYRGVVTNTA 797
QY 903 CGCTACTTTAGCCAAATAATGTAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 857
Db 798 ARDGNWNN 815
QY 963 AGCAACTAATGTAATTAATAACAGAAATGCTAAATG-----TGCTGCTAACT 1015
Db 858 DDRWRBAYTNN 917
QY 1016 TTTATTTTGTAGTAAATATTTAGCAGGAAGTAGTAGTACGCAAGCATGTCCAGCAA 1075
Db 918 NNN 977
QY 1076 ATAAAGTTTAAAGGCGCTGTAGCAACTGCAGGTGGTACTGCTACTTTTAAATGCAATG 1135
Db 978 CTWYTWMTTTRTYAATRWKTNATGSMTRCNATGKNNNNYTWGKTRWTFAYRMAFRM 1037
QY 1136 CCCTTGAATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1195
Db 1038 KAWWYKATGWSWNTSYARWATKTRAYKGWYNNACAWRWKWKATCYMTDANWWTACATS 1097
QY 1196 CAGCATCTGAATGCTGTTAAATGCTGCTGCAA 1226
Db 1098 WMAHKNWMMCKNN 1128

RESULT 9
US-10-017-161-1913
; Sequence 1913, Application US/10017161
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI

; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1913
; LENGTH: 3532
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: source
; LOCATION: (1)..(3532)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (201)..(437)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2622)..(3332)
; US-10-017-161-1913

Query Match 3.4%; Score 48; DB 6; Length 3532;
Best Local Similarity 44.0%; Pred. No. 0.19;
Matches 204; Conservative 0; Mismatches 260; Indels 0; Gaps 0;

QY 513 TCATGATGGAGTAACACTACTGATTATGTAGATCATTCACAGAAATGTGTTAAATGATGACT 572
Db 2639 TGTGTGTTGTTGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 2698
QY 573 TAACTTTTACTAATGTTAAATGTTAAATGTTAAATGTTAAATGTTAAATGTTAAATGTT 632
Db 2699 TGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2758
QY 633 CACACCTTGTCCGGCAATTTAAACCTGCTAATGTTGCTTAAAGCTACTTTTAGTAAATGATGC 692
Db 2759 TGTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2818
QY 693 TACAATAACCGCATATGTAAGCTTGCATGCCCTGATGCTACTTAAGTCTGCTGCTGCTGCTG 752
Db 2819 TGATGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2878
QY 753 AAATAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 812
Db 2879 TGATAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2938
QY 813 TAATGCTCTTAATTTCAATCCAGGTAAATAGTACATGCCCTACCTTGCCTGCTGCTGCTGCTG 872
Db 2939 TGACGGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2998
QY 873 TTAGTGTCTGAAGCCACTGCAGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 932
Db 2999 TGATGTTGATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3058
QY 933 ATGCCCTGATGTTGCTCAATTCCTAGTGAGCAACTAATTAATG 976
Db 3059 TGTGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 3102

RESULT 10
US-10-144-771-4707/G
; Sequence 4707, Application US/10144771
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
; FILE REFERENCE: CL001321
; CURRENT APPLICATION NUMBER: US/10/144,771
; CURRENT FILING DATE: 2002-05-15
; NUMBER OF SEQ ID NOS: 47235
; SEQ ID NO 4707

PRIOR FILING DATE:	04 February 2000	(04.02.00)
PRIOR APPLICATION NUMBER:	US 60/207,456	
PRIOR FILING DATE:	26 May 2000	(26.05.00)
PRIOR APPLICATION NUMBER:	US 09/632,366	
PRIOR FILING DATE:	03 August 2000	(03.08.00)
PRIOR APPLICATION NUMBER:	GB 24263.6	
PRIOR FILING DATE:	03 October 2000	(03.10.00)
PRIOR APPLICATION NUMBER:	US 60/236,359	
PRIOR FILING DATE:	27 September 2000	(27.09.00)
PRIOR APPLICATION NUMBER:	US 60/234,687	
PRIOR FILING DATE:	21 September 2000	(21.09.00)
PRIOR APPLICATION NUMBER:	US 09/608,408	
PRIOR FILING DATE:	30 June 2000	(30.06.00)
NUMBER OF SEQ ID NOS:	15438	
SOFTWARE:	Molecular Dynamics Sequence Listing Engine	
SEQ ID NO	2529	
LENGTH:	1403	
TYPE:	DNA	
ORGANISM:	Homo sapiens	
FEATURE:		
OTHER INFORMATION:	MAP TO AL078472.1	
FEATURE:		
OTHER INFORMATION:	EXPRESSED IN BT474, SIGNAL = 34	
US-10-203-138A-2529		
Best Match	3.2%; Score 45.8; DB 6; Length 1403;	
Best Local Similarity	41.7%; Pred. No. 0.53;	
Matches	287; Conservative 0; Mismatches 402; Indels 0; Gaps	
QY	288 TCCTGGTACCCCAATTCCAGGTGAGCAACAGATTTATGCAGCAATAATCACAGAATCGTG 347	
Ddb	566 TCATGGTGGTCATGGTGGTGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 625	
QY	348 TAATTGTAGATTAAATTTTATATGAATAATGCTCCAATAATTTAATGCAGGTGCCTAGTAC 407	
Ddb	626 TGGTGATGGTGGTGATGGTAGTGGTGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGA 685	
QY	408 ATGCACAGCTTTGCCGGTAACAGAGTTGGTGGTGATGTGACPGCTGGTAATGACCGCTAC 467	
Ddb	686 TGGTGGTGGTGATGGTGGTGATGCTAGCTGGTGGTAGTGGTACTGGTGGTGGTGGTGGTGA 745	
QY	468 CATATGCCATAATGTAACTGCATCTCCTACTGGTACTGCCTTGCCTTGCCTTGCCTTGCCTAAC 527	
Ddb	746 TGGTGGTGGTGCTGGTGATGGTGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 805	
QY	528 TACTGATTATGTTAGATCATTCACAGAAATGTTTAAATGTAGACTTAACTTTTACTATATAA 587	
Ddb	806 TGGTGGTAGTGGTAGTGGTGATGGTGGTGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 865	
QY	588 TGGTAATAATGGTAATATCTCTTTCAATCCAGGTAAAAGTTAATGCACACCTTGTCCTGGC 647	
Ddb	866 TGGTGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 925	
QY	648 AATTAAACCTGCTAATGTTCCTTAAGCTACTTTAGTAATGATGCTACAATAACCACATA 707	
Ddb	926 TAGTGGTGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 985	
QY	708 ATGTAACGTTGCATGCCCTGATGGTACTATAAGTGTGCTGGAGCTAAATAATTTGGGTAGC 767	
Ddb	986 TGGTGGTGGTGTAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1045	
QY	768 ACMAAACACTGAATGTACTAATTTGGTCCCTAACTTTTTACAAATAAATGCTCCTCAATTT 827	
Ddb	1046 TGGTGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1105	
QY	828 CAATCCAGCTAATAGTACATGCCTACCTTGCCTGCCAGCAAATAAAGATTATGGTCTGAAGC 887	
Ddb	1106 TGATGG 1165	
QY	888 CACTCAGGTGGTGGCGCTACTTTTAGCCAAATAATGTAATAATTCATGCCCTCATGGTAC 947	
Ddb	1166 TCATGG 1225	

[illegible]

RESULT 14

RESULT 14
UIC-10-092-411A-22A3

US-10-092-411A-2243
sequence 2243. Application US/10092411A

; Sequence 2243, Appl. : GENERAL INFORMATION:

ADDICANT: Lynn Doucette-Stamm et al

APPLICANT: LYNN DOUGLASS STAMMER et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES;
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

; TITLE OF INVENTION: EPIDEMIOLOGICAL SURVEILLANCE OF
; FILE REFERENCE: 032796=101

FILE REFERENCE: 032796-101
CURRENT APPLICATION NUMBER: IIS/10/092.411A

CURRENT APPLICATION NUMBER: US/1
 CURRENT FILING DATE: 2002-03-07

; CURRENT FILING DATE: 2002-03-07
 ; PRIOR PUBLICATION NUMBER: US 09/134,001

; PRIOR APPLICATION NUMBER: US 09/134,001
 ; PRIOR FILING DATE: 1998-08-13

; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5676
; SEQ ID NO 2243
; LENGTH: 11091
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-10-092-411A-2243

Query Match 3.2%; Score 45.8; DB 6; Length 11091;
Best Local Similarity 46.9%; Pred. No. 0.71;
Matches 143; Conservative 0; Mismatches 162; Indels 0; Gaps 0;
Qy 736 TGATGGTACTAAGTCTGCTGGAGTAATAATTTGGGTAGCACAAACACTGAATGTAC 785
Db 3906 TGATGGTATTGTGATGGTACAGCAAGCAATAAATTCGAATTTACACCTGATACATCAAT 3965
Qy 786 TAATTTGCTCTAACTTTTACAAATAATGCTCCTAAATTTCAATCCAGGTAATAGTAC 845
Db 3966 TAAAGAAATGCTAAAATGATTTGATATTAAAGCAGCTGATAAGAAAATAAAAATTC 4025
Qy 846 ATGCTACCTTGGCCACCAATAAAGATTATGCTGTAAGCCACTGCAGGTGGTCCGC 905
Db 4026 AAGAAATAATGATGCTACAGATGAAGAAATTCAGAAAGCAATCGTAAAATTTGAAGAC 4085
Qy 906 TACTTTAGCCAAATAATGTAATATTCATGCTCCCTGATGGTACTGCTGCAATTTGCTAGTGGAGC 965
Db 4086 TAAGATTGAAGCAAGATAATTTCAACGCAATAGTACTAGAGATCAAGATAAATGAAGC 4145
Qy 966 AACTAATTTGTAATATTATAAACAAGATGCTTAAATTTGCTGCTAACTTTTATTTTGA 1025
Db 4146 GAAACTAATGGAATAAATAAATAGAAAATAAATACACCACTACTGTGAATCTGA 4205
Qy 1026 TGTA 1030
Db 4206 AGCTA 4210

RESULT 15
US-09-949-004-601
; Sequence 601, Application US/09949004
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTOR GENES ASSOCIATED WITH DISEASE, METHODS OF DETECTION
; FILE REFERENCE: CL000848
; CURRENT APPLICATION NUMBER: US/09/949,004
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 60/232,045
; PRIOR FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 6961
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 601
; LENGTH: 21423
; TYPE: DNA
; ORGANISM: Human
US-09-949-004-601

Query Match 3.2%; Score 45; DB 5; Length 21423;
Best Local Similarity 45.4%; Pred. No. 1.2;
Matches 250; Conservative 0; Mismatches 290; Indels 11; Gaps 2;
Qy 498 TACTGTCTGCTGACTGATGGAGTAAGTACTGATTGTTAGATCATTTCACAGAAATG 557
Db 19722 TAATGCTGATGTTGATGAGGTGATATGATGAAGATGATATAAGGTAATGAAT 19781
Qy 558 TGTTAATCTAGACTTTACTTTTACTATAATGGTAATATGTTAACTCTCTTTCAATCC 617
Db 19782 TGATGATGTTGAAGGTGATGGTAAATGGTATGATGGTGAAGGTGATGATGAAGATGATGA 19841

Qy 618 AGGTAAAAAGTTAATGCACACACCTTCTCGGCAATTTAAACCTGCTAATGCTTCTTAAGCTAC 677
Db 19842 CAATGAAGGTGATGATAGTATGATGATGGTGAAGGTGATGATGATGAAGTTGATGATAA 19901
Qy 678 TTTAGGTAATGATGCTACATAACCCGCAATATGTAAGCTTTGGCATGCCCTGATGGTACTAT 737
Db 19902 TGGAACGACGATGTTAAAAAGTAGCGTGATGATTAAAAATGATCATGATGAGGCTGATGA 19961
Qy 738 AAGTCTGCTGGAGTAAATAATTTGGGTAGCACAAACACTGAATGTACTAATTTGTCTCC 797
Db 19962 TGGTGAATTTGATGAAGGTGATGTTAGTGAAGGTGATGATGAAGGTGATGGTATGGTGG 20021
Qy 798 TAACTTTTACAAATAATCTCCTCAATTTTCA--ATCCAGGTAATAGTACATGCCCTACCT 855
Db 20022 TGATAGTATGATGATGAAAGTAAATGTGAAGGTGATGATGAAGGTGATGATGATGATGAT 20081
Qy 856 TGCCACAGCAATAAAGATTATGCTGCTGAAGCCACTGCAGGTGGTCCCTACTTTAGCC 915
Db 20082 GGTGATAGTATGATGATGGTGGTGGTGA-----TGGTATGGTGGTATGATGAAGAT 20132
Qy 916 AAATAATTAATATTGTCATGCCCTGATGGTACTGCAATTTGCTAGTGGAGCAACTAATAT 975
Db 20133 GATGAAGGTGATGATGGTGAAGGTGATGATTATAAGGTGATGGTGGTATCACAGTATGAT 20192
Qy 976 GTATATTTATAACACAGTAATGCTCTAAATTTGCTGCTGCTAACTTTTATTTTGGTATGAT 1035
Db 20193 GATAAAGGTGATAATGAAGGTTATGGTAATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 20252
Qy 1036 TTCTAGGCAGG 1046
Db 20253 GATGATGAAGG 20263

Search completed: February 17, 2003, 01:55:34
Job time : 243.042 secs

